

AMENDMENTS TO THE DRAWINGS

Please replace Fig. 13 with the Replacement Sheet for Fig. 13.

REMARKS

1. Formal Matters

a. Status of the Claims

Claims 1-22 are pending in the instant application. Claims 1-22 are hereby canceled without prejudice to pursuing the canceled subject matter in a continuing application; and claims 23-38 are new. Upon entry of these amendments, claims 23-38 are pending and under active consideration. Applicant respectfully requests entry of the amendments and remarks made herein into the file history of the instant application.

b. Amendments to the Claims

New claim 23 recites a nucleic acid consisting of 19 to 140 nucleotides, support for which can be found at paragraphs 0046, 0049, and 0050 of the specification as originally filed. Paragraph 0046 in part recites, "An 'Oligonucleotide' is defined as a nucleic acid comprising 2-139 nts, or preferably 16-120 nts." Paragraph 0049 in part recites, "an oligonucleotide having a nucleotide sequence that is 50-140 nts in length..." Paragraph 0050 in part recites, "an oligonucleotide which is about 19 to about 24 nts in length..." Accordingly, the specification as originally filed discloses oligonucleotides ranging in length from 19 to 140 nucleotides.

New claim 23, part (a) recites that the sequence of the nucleic acid comprises SEQ ID NO: 348, support for which can be found at paragraph 0055 of the specification as originally filed. New claim 23, part (b) recites an RNA equivalent of (a), support for which can be found at paragraph 0030 and Table 1, line 778 of the application as originally filed. Paragraph 0030 in part recites, "the present invention relates to a novel group of 4,363 bioinformatically detectable human regulatory RNA oligonucleotides..." Table 1 discloses that the sequence as set forth in SEQ ID NO: 348 is from a human, as follows:

GAM SEQ-ID	GAM NAME	GAM RNA SEQUENCE	GAM ORGANISM	GAM POS
=====	=====	=====	=====	=====
348	GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	A

New claim 23, part (c) recites a sequence at least 63.7% identical to (a) or (b), support for which can be found at Table 7, lines 312839-313772 as originally filed. Table 7 discloses that 15 out of 22 nucleotides (63.7%) of SEQ ID NO: 348 (GAM353678) are sufficient for binding target mRNAs. For example, 63.7% of the residues of SEQ ID NO: 348 are capable of targeting mRNAs of the human gene SERPINH1, as follows:

GAM NAME	GAM ORGANISM	GAM RNA SEQUENCE	TARGET BS-SEQ	TARGET SERPINH	TARGET REF-ID	TARGET ORGANISM	UTR	BINDING SITE (UPPER:TARGET;LOWER:GAM)	DRAW	GAM POS
=====	=====	=====	=====	=====	=====	=====	=====	=====	=====	=====
GAM353678	Human	CAGCAGCA CACTGTGG TTTGTA	AAACTAGG TGCTGCAG 1	SERPINH	NM_001235	Human	3	--- G --- AAACTA G TTTGGT T ATG G CAC	A TGCTGC G ACGACG C A	A

New claim 23, limitation (d) recites the complement of any one of (a)-(c), support for which can be found at paragraph 0035 of the specification as originally filed.

New claim 24 recites the nucleic acid of claim 23, wherein the sequence of the nucleic acid comprises SEQ ID NO: 4233864, support for which can be found at Table 1, line 778 and Table 5, line 1276 of the application as originally filed. Table 5 discloses that SEQ ID NO: 4233864 is the precursor of SEQ ID NO: 348 as follows (See the column "PRECURSOR SEQ-ID"):

GAM NAME	GAM ORGANISM	GAM RNA SEQUENCE	PRECUR SEQ-ID	GAM POS
=====	=====	=====	=====	=====
GAM353678	Human	CAGCAGCACACTGTGGTTTGTA	4233864	A

Table 1, as shown above, discloses that the sequence as set forth in SEQ ID NO: 348 is the sequence of GAM353578 shown in Table 4 (See the column "GAM RNA SEQUENCE").

New claim 25 recites the nucleic acid of claim 23, wherein the sequence of the nucleic acid consists of (a) SEQ ID NO: 348, (b) an RNA equivalent of (a), a sequence at least 63.7% identical to (a) or (b), or the complement of any one of (a)-(c), support for which can be found as described above for new claim 23.

New claim 26 recites the nucleic acid of claim 23, wherein the sequence of the nucleic acid consists of SEQ ID NO: 4233864, support for which can be found as described above for new claim 24.

New claim 27 recites the nucleic acid of claim 23, wherein (c) is a sequence at least 77.3% identical to (a) or (b), support for which can be found at Table 7, lines 312839-313772 as originally filed. Table 7 discloses that 17 out of 22 nucleotides (77.3%) of SEQ ID NO: 348 (GAM353678) are sufficient for binding target mRNAs. For example, 77.3% of the residues of SEQ ID NO: 348 are capable of targeting mRNAs of the gene uhpA of *Yersinia pestis*, as follows:

GAM353678	Human	CAGCAGCA	CAGCGCTT	uhpA	NC_003143	f	Yersinia pes	3	--	CG T	A	A
		CACTGTGG	GGTGATGC		rom	45227	tis			CAG C	TGGTG TGCTGCTG	
		TTTGTA	TGCTG		90 to	45233				GTT G	GTCAC ACGACGAC	
					80	(-)				AT	TG T	-

New claim 28 recites the nucleic acid of claim 25, wherein (c) is a sequence at least 77.3% identical to (a) or (b), support for which can be found as described above for new claim 27.

New claim 29 recites the nucleic acid of claim 23, wherein (c) is a sequence at least 86.4% identical to (a) or (b), support for which can be found at Table 7, lines 312839-313772 as originally filed.

Table 7 discloses that 19 out of 22 nucleotides (86.4%) of SEQ ID NO: 348 (GAM353678) are sufficient for binding target mRNAs. For example, 86.4% of the residues of SEQ ID NO: 348 are capable of targeting mRNAs of the gene *cysQ* of *Pseudomonas putida* KT2440, as follows:

GAM353678 Human	CAGCAGCA CAGGCGCA <i>cysQ</i>	NC_002947 f <i>Pseudomonas</i>	3 -- G G	A
	CACGTGTGG GGGTGTGC	rom 3151 <i>putida</i> KT244	CAGGC CA GGTGTGCTGCTG	
	TTTGTA TGCTG	84 to 31598 0	GTTTG GT TCACACGACGAC	
		4 (+)	AT - G	

New claim 30 recites the nucleic acid of claim 25, wherein (c) is a sequence at least 86.4% identical to (a) or (b), support for which can be found as described above for new claim 29.

New claim 31 recites a vector comprising the nucleic acid of claim 23, support for which can be found at paragraph 0045 of the application as originally filed, which recites in part, "... 'Isolated Nucleic Acid'... [is] defined as a nucleic acid that is free of the genome of the organism from which the nucleic acid is derived, and include[s], for example, a recombinant nucleic acid which is incorporated into a vector..."

New claim 32 recites a vector comprising the nucleic acid of claim 24, support for which can be found as described above for new claim 31.

New claim 33 recites a vector comprising the nucleic acid of claim 25, support for which can be found as described above for new claim 31.

New claim 34 recites a vector comprising the nucleic acid of claim 26, support for which can be found as described above for new claim 31.

New claim 35 recites a vector comprising the nucleic acid of claim 27, support for which can be found as described above for new claim 31.

New claim 36 recites a vector comprising the nucleic acid of claim 28, support for which can be found as described above for new claim 31.

New claim 37 recites a vector comprising the nucleic acid of claim 29, support for which can be found as described above for new claim 31.

New claim 38 recites a vector comprising the nucleic acid of claim 30, support for which can be found as described above for new claim 31.

c. Amendments to the Specification

A number of paragraphs throughout the specification are amended to assign SEQ ID NOs to the sequences shown in Figures 14B, 15A, and 17C, and to sequences which are listed in the paragraphs in compliance with 37 C.F.R. §§ 1.821-1.825.

d. Amendments to the Drawings

Figure 13 is amended by replacing it with a Replacement Sheet for Fig. 13 to assign SEQ ID NOs: 4254671-4254759 to the listed sequences in compliance with 37 C.F.R. §§ 1.821-1.825.

e. Specification/Sequence Compliance

On page 2 of the Office Action, the Examiner objects to the application because it allegedly contains nucleotide sequences of over 10 nucleotides each that are not identified by accompanying sequence identifiers. The Examiner asserts that the sequences set forth at paragraphs 0286, 0302, 0303, and 0330, and some sequences in Figures 13-15 do not contain sequence identifiers.

Applicant respectfully submits that the specification and drawings are amended to disclose the appropriate SEQ ID NOs in compliance with 37 C.F.R. §§ 1.821-1.825. In view of the foregoing amendments and remarks, Applicant respectfully requests that the Examiner reconsider and withdraw the objection to the application for allegedly not complying with the sequence rules.

2. Election**a. Restriction to a single invention**

On pages 3-10 of the Office Action, the Examiner requires restriction to one of Groups I-XVI, as set forth on pages 3-7 of the Office Action, under 37 C.F.R. § 121. Applicant elects without traverse Group I, which is now considered claims 23-38, drawn to an isolated nucleic acid and a vector comprising the nucleic acid.

b. Restriction to a single nucleotide sequence and mRNA target gene

On pages 10-12, the Examiner requires further restriction to one SEQ ID NO and one target gene under 35 U.S.C. § 121. Applicant without traverse elects SEQ ID NO: 348, which is associated with claims 23-38, and the human target gene SERPINH1.

3. Conclusion

Applicant respectfully submits that the instant application is in good and proper order for allowance and early notification to this effect is solicited. If, in the opinion of the Examiner, a telephone conference would expedite prosecution of the instant application, the Examiner is encouraged to call the undersigned at the number listed below.

Respectfully submitted,

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